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? show files
File 155:MEDLINE(R) 1966-2004/Jun W2
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File   5:Biosis Previews(R) 1969-2004/Jun W4
         (c) 2004 BIOSIS
File  35:Dissertation Abs Online 1861-2004/May
         (c) 2004 ProQuest Info&Learning
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         (c) 2004 The Gale group
File  71:ELSEVIER BIOBASE 1994-2004/Jun W3
         (c) 2004  Elsevier Science B.V.
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         (c) 2004 Thomson Derwent & ISI
File 358:Current BioTech Abs 1983-2004/May
         (c) 2004 DECHEMA
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Set     Items   Description
S2     884187   (PROTEIN OR PEPTIDE? ? OR POLYPEPTIDE? ?)(5N)(DESIGN OR PR-
             EPARATION OR GENERATE OR GENERATION OR ENGINEER? OR MANUFACTU-
             R? OR PRODUC? OR SYNTH?)
S3      87487   (CAMD OR CAD OR COMPUTER(W)(AIDED OR ASSISTED)(2N)DESIGN)
S4      73732   (BIND OR BINDING OR ATTACH?)(5N)TERMI?
S5         15   S2 AND S3 AND S4
S6          9   RD (unique items)
S7          5   S6 NOT CALDESMON
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 7/AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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10261806   PMID: 7525561
  Identification  of the regulatory domain of the mammalian multifunctional
protein CAD by the construction of an Escherichia coli hamster hybrid
carbamyl-phosphate synthetase.
  Liu X; Guy H I; Evans D R
  Department  of  Biochemistry,  Wayne State University School of Medicine,
Detroit, Michigan 48201.
  Journal  of biological chemistry (UNITED STATES)  Nov 4 1994,  269  (44)
 p27747-55,  ISSN 0021-9258  Journal Code: 2985121R
  Contract/Grant No.: GM 47399; GM; NIGMS
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: Completed
  Carbamyl-phosphate synthetases from different organisms have similar
catalytic mechanisms and amino acid sequences, but their structural
organization, sub-unit structure, and mode of regulation can be very
different. Escherichia coli carbamyl-phosphate synthetase (CPSase), a
monofunctional  protein  consisting  of  amido-transferase  and
synthetase subunits, is allosterically inhibited by UMP and activated
by  NH3,  IMP, and ornithine. In contrast, mammalian CPSase II, part of the
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                  D? OR ?ATTACH?)
L11        117189 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L5(L)L10
L12           771 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L9 AND L11
L13       1068575 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L3 OR 'IN SILICO' OR GLASS
L14            10 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L12 AND L13
L15            10 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L14 NOT L2
L23           287 SEA FILE=HCAPLUS ABB=ON  PLU=ON  ENGINEERED (L)PROTEIN(L)BINDIN
                  G(L)DOMAINS
L24             8 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L23 AND L7
L25             7 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L24 NOT (L2 OR L15)
L26          2882 SEA FILE=HCAPLUS ABB=ON  PLU=ON  COMPUTER(W)(ASSISTED OR
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L27           251 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L26 AND L5
L28            16 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L27 AND L11
L29            14 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L28 NOT (L2 OR L15 OR L25)
L30           277 SEA FILE=HCAPLUS ABB=ON  PLU=ON  COMPUTER(W)(ASSISTED OR
                  AIDED)(W)DRUG(W)DESIGN
L31             8 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L29 NOT L30

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=> d ibib abs hitrn l31 1-8

L31  ANSWER 1 OF 8  HCAPLUS  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:         2001:303055  HCAPLUS
DOCUMENT NUMBER:          135:101926
TITLE:                    Design of inhibitors of Ras-Raf interaction using a
                          computational combinatorial algorithm
AUTHOR(S):                Zeng, Jun; Nheu, Thao; Zorzet, Anna; Catimel, Bruno;
                          Nice, Ed; Maruta, Hiroshi; Burgess, Antony W.;
                          Treutlein, Herbert R.
CORPORATE SOURCE:         Ludwig Institute for Cancer Research, Royal Melbourne
                          Hospital, Parkville, 3050, Australia
SOURCE:                   Protein Engineering (2001), 14(1), 39-45
                          CODEN: PRENE9; ISSN: 0269-2139
PUBLISHER:                Oxford University Press
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
AB   Drugs that inhibit important protein-protein
     interactions are hard to find either by screening or rational design, at
     least so far.  Most drugs on the market that target proteins
     today are therefore aimed at well-defined binding pockets in
     proteins.  While computer-aided design
     is widely used to facilitate the drug discovery process for binding
     pockets, its application to the design of inhibitors that target the
     protein surface initially seems to be limited because of the
     increased complexity of the task.  Previously, we had started to develop a
     computational combinatorial design approach based on the well-known
     "multiple copy simultaneous search" (MCSS) procedure to tackle this
     problem.  In order to identify sequence patterns of potential inhibitor
     peptides, a three-step procedure is employed: first, using MCSS,
     the locations of specific functional groups on the protein
     surface are identified; second, after constructing the peptide
     main chain based on the location of favorite locations of
     N-methylacetamide groups, functional groups corresponding to amino acid
     side chains are selected and connected to the main chain Cα atoms;
     finally, the peptides generated in the second step are aligned
     and probabilities of amino acids at each position are calculated from the
     alignment scheme.  Sequence patterns of potential inhibitors are determined
     based on the propensities of amino acids at each Cα position.  Here
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